

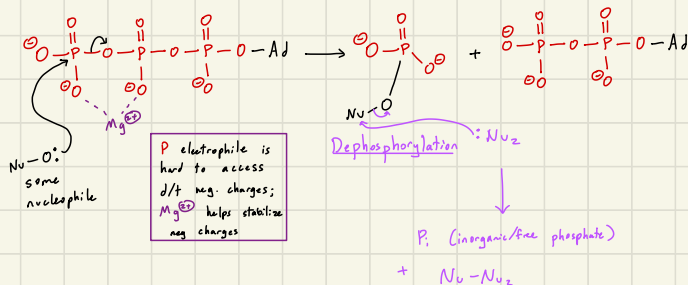
Phosphorylation

(from prior exam notes)

Phosphate Bonds

Thermodynamically favorable $\Delta G \ll 0$

Kinetically unfavorable d/t neg charges
(needs Mg^{2+} to lower E_a)



can also stabilize other \ominus eg HO^- in other enzymes

Names

ATP = ad - 3 phosphates

ADP = ad - 2 phosphates

AMP = ad - 1 phosphate

P_i = free PO_4^{3-}

PP_i = free $P_2O_7^{4-}$

Enzyme Names!

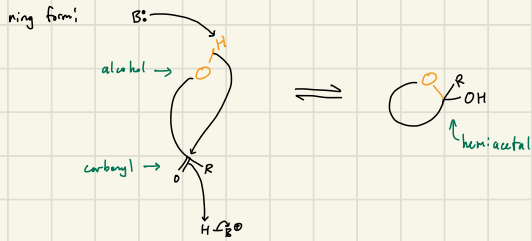
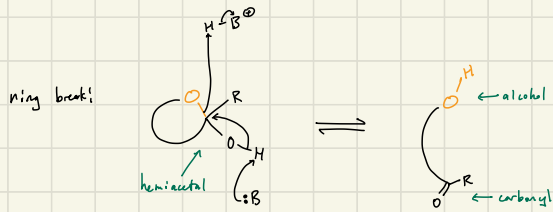
Kinase

Phosphorylase (add P_i)

Phosphatase (remove P_i)

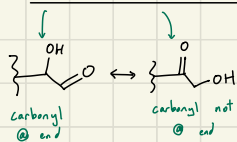
Ring break/form (aka hemiacetal formation = connect/disconnect C-O bond)

(Chem 17 review)



No specific enzyme names

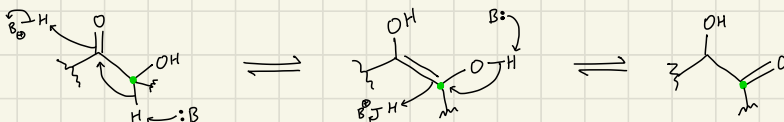
Aldose-Ketose Isomerization



carbonyl not @ end



carbonyl @ end



① OHs carbon deprotonated
→ double bond,
carbonyl → another new OH

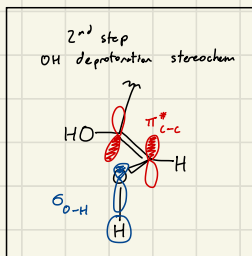
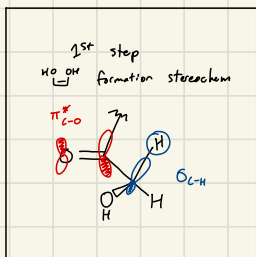
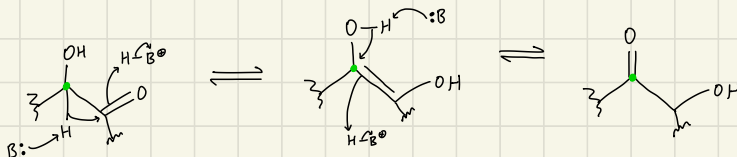
② old OH → new carbonyl,
double bond re protonated
→ single bond

carbonyl @ end



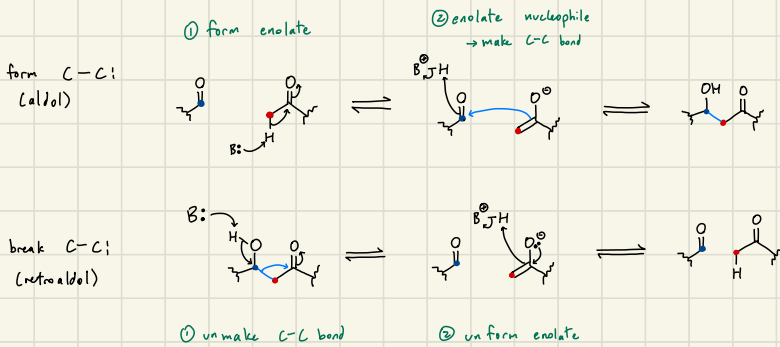
carbonyl not @ end

other
direction:

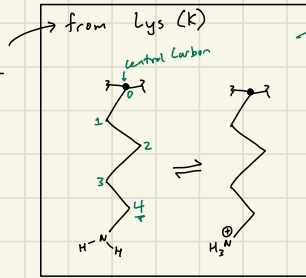


Enzymes!
Isomerase

Aldol/Retro-Aldol = connect/disconnect C-C bond



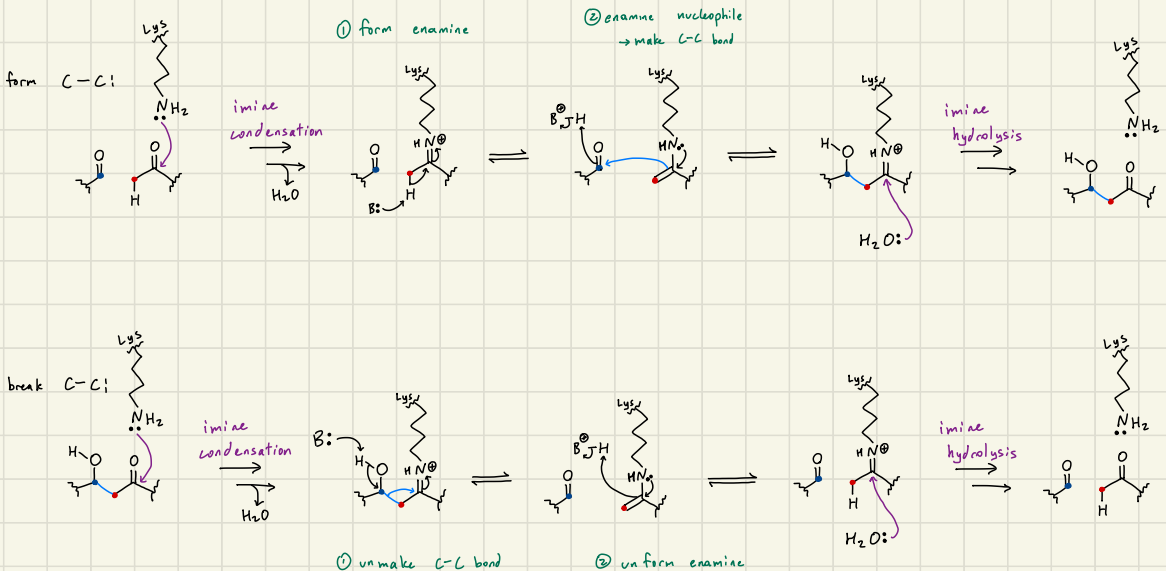
Aldol/Retro-Aldol w Imine



Why w imine?

form C-C:
avoid neg charge O^- OH (not good nuc)
use enamine N^- enol nuc instead

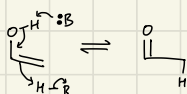
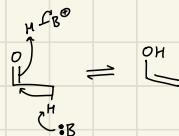
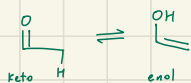
break C-C:
imine N^+ $\text{better electroph. than}$ C=O



Enzymes:
Aldolase

Keto-enol Tautomerization

from chem17

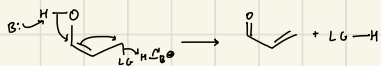
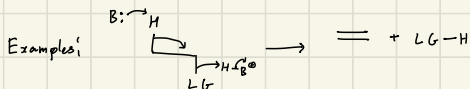


E1cb mechanism

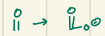
eliminate something using
extra e^- for double bond formation

from Chem17

no specific
enzymes

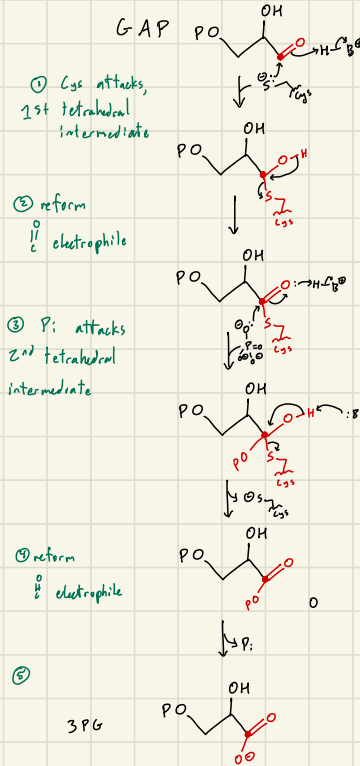


GAPDH



oxidation

with Cys & P_i



GAPDH

& a few other
Dehydrogenases

Decarboxylation

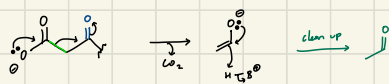
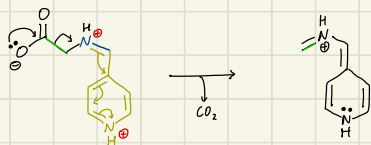
Chem17

CO₂ leaves via pushing old C-C bond e⁻ onto good e⁻ sink: eg \oplus charge,

resonance,

good electrophiles

ex.



clean up

